

FIGURE 1

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCAGCGGTGGGGAGGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCTCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCCGGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCGGGGGCCGGAGGGGCTGGGCTGGGCCGGAGGCAG
GGTGTGAGTGGGTGTGCGGGGGCGGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGGCGCGCCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTTGGTCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGGCGCCCTCGCCTTCGGACGCCGGCC
CCACGTGCACTACGGCTGGGGCGACCCCCTCCGCCTGCCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCCGCATCCGTGCCGACGGCGTGTGGACTGCCGCGGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTTGCGGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTGCACAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAG**TAA**CT
GAGACCATGCCGGCCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCTAGCTAGCAATAGACTTGTCTGAT
CATAAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCCATTCTGCTCCCTGA
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTTGAATAACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAATCTTATGTCAAGCTGAATTCTCTAATTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGGAAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGGATTGATCTATATCTACTTCCAGGG
ACCATTGCCCTTCCCAAATCCCTCAGGCCAGAACAGTGAACGGAGCAGGCATGGCCACCCAG
GCTTCAGGAGTAGGGGAAGCCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCACTGGATGCTGCTGAGAATAACTTGCTGCTGCCGTGTCACCTGC
TTCCATCTCCAGCCACCCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGG
CCCAGGCCCCCAGCTTATGTCAACCTGCACTTCTGTTCAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTTGGAGCAGCGGGGGAGACCTAGAAC
CCTTCCCCAGCACCTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCCAAATTATATTATGATGTAAAGTGGAGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 2

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

signal peptide:
amino acids 1-22

N-myristoylation sites:
amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site:
amino acids 48-59

HBGF/FGF domain:
amino acids 80-131

FIGURE 3A

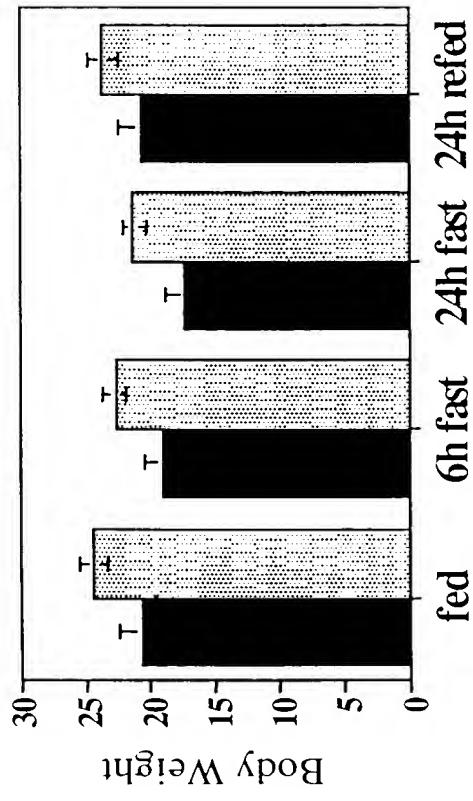


FIGURE 3B

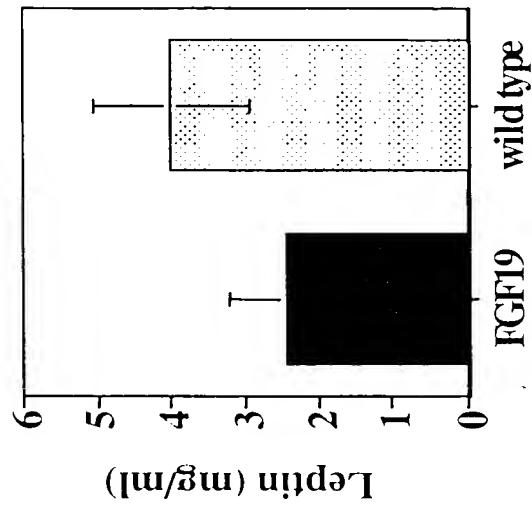


FIGURE 4A

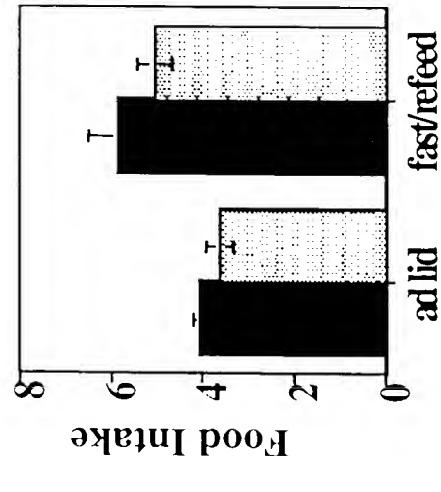


FIGURE 4B

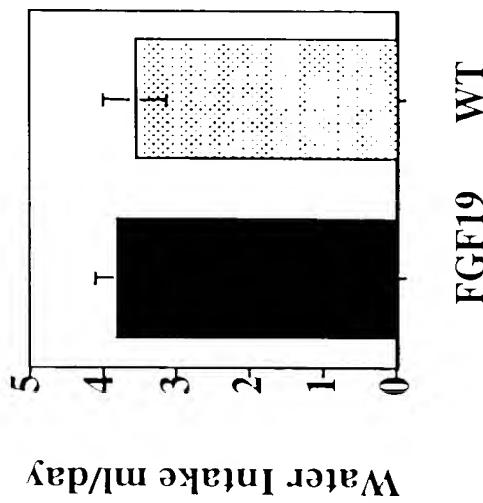


FIGURE 4C

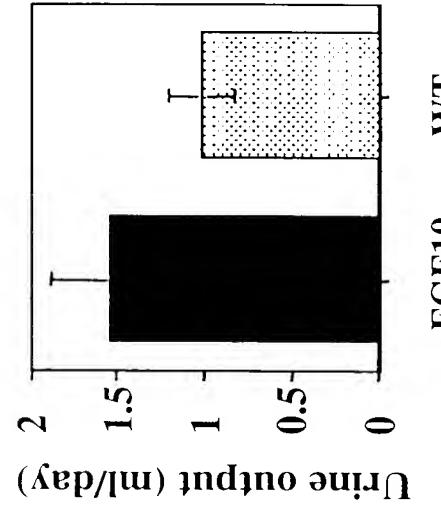


FIGURE 4D

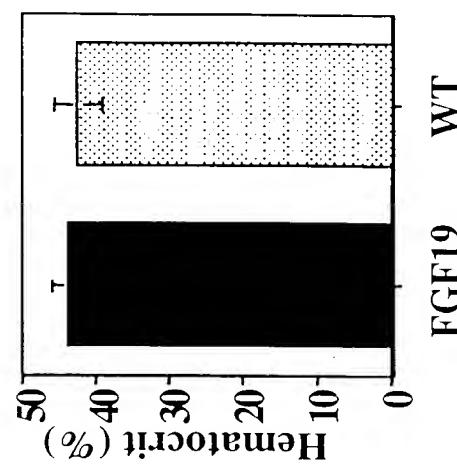


FIGURE 5

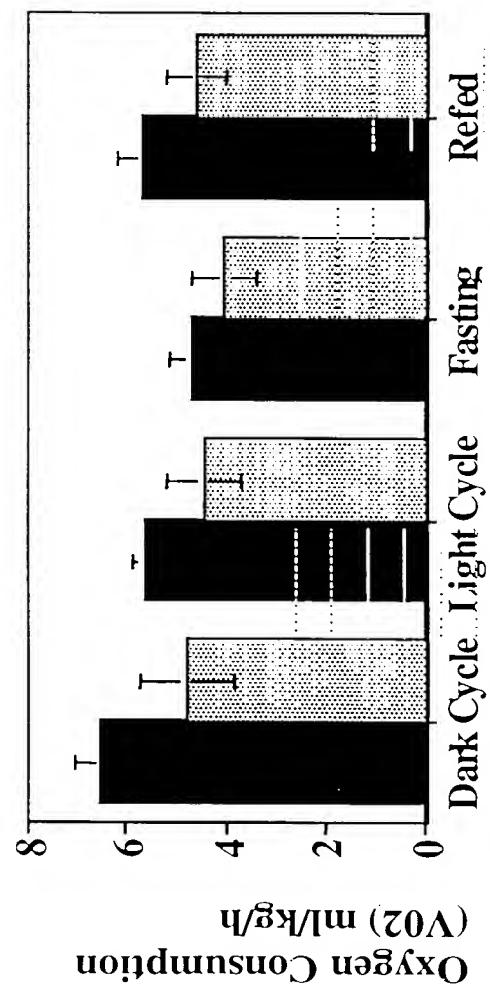


FIGURE 6A

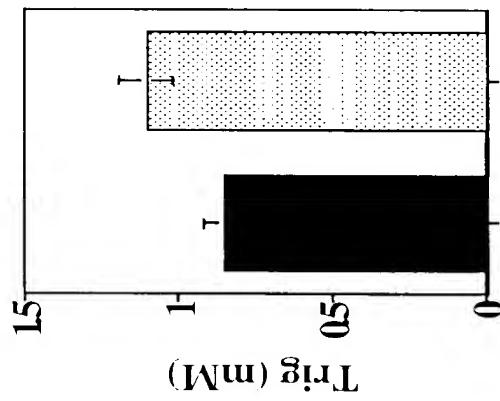


FIGURE 6B

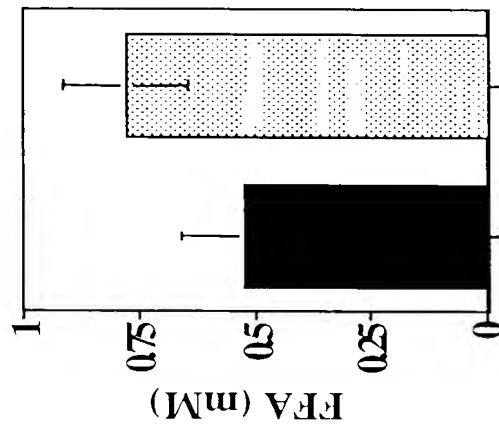


FIGURE 7A

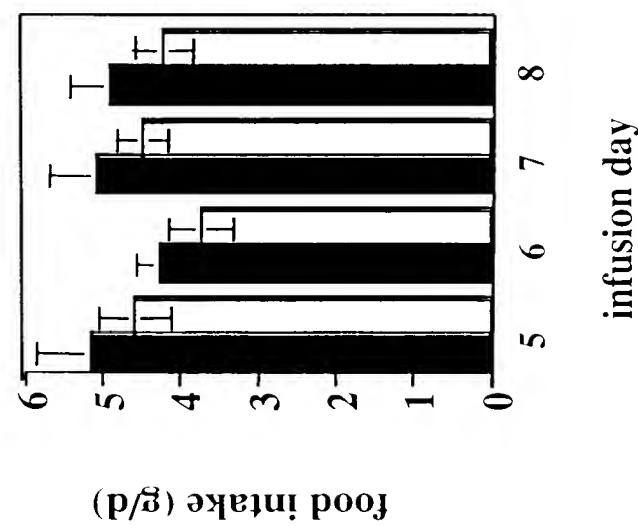


FIGURE 7B

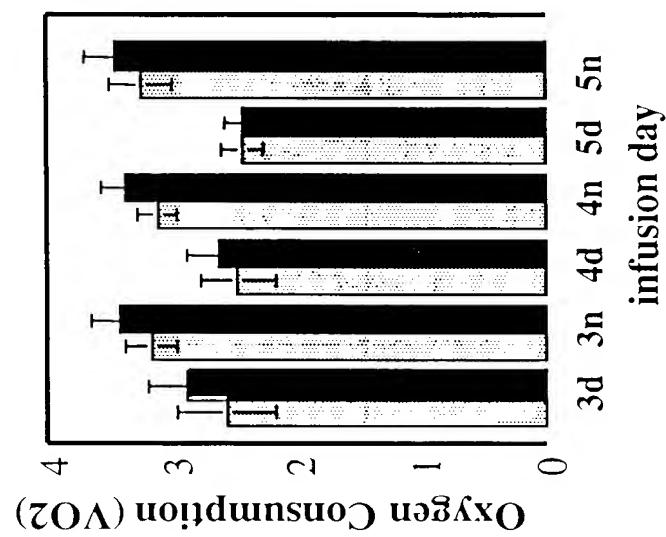


FIGURE 8A

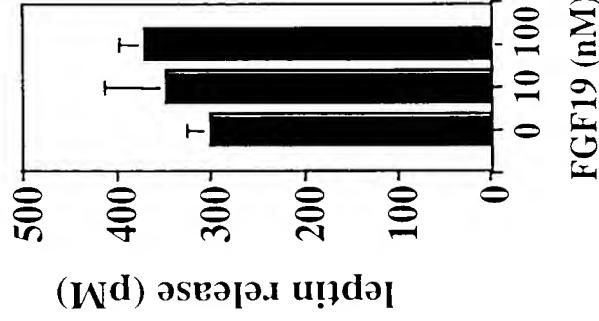
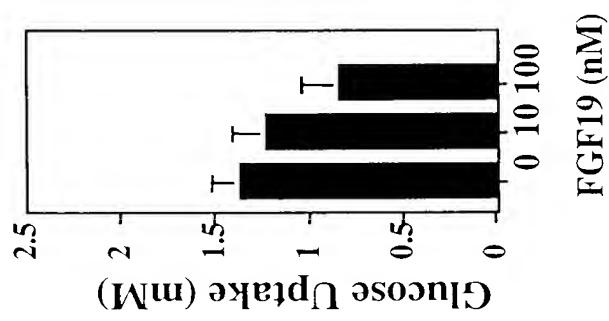


FIGURE 8B



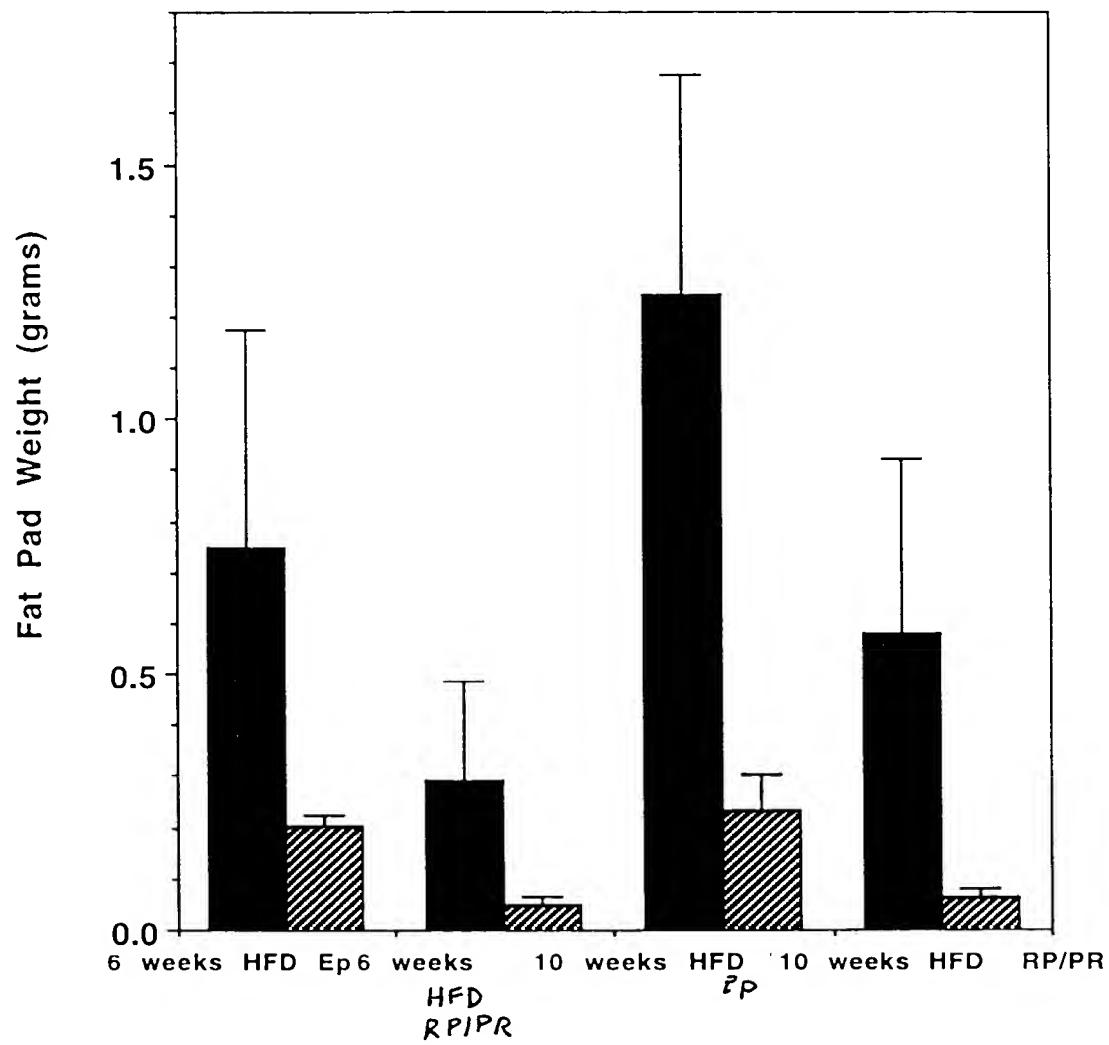


FIGURE 9

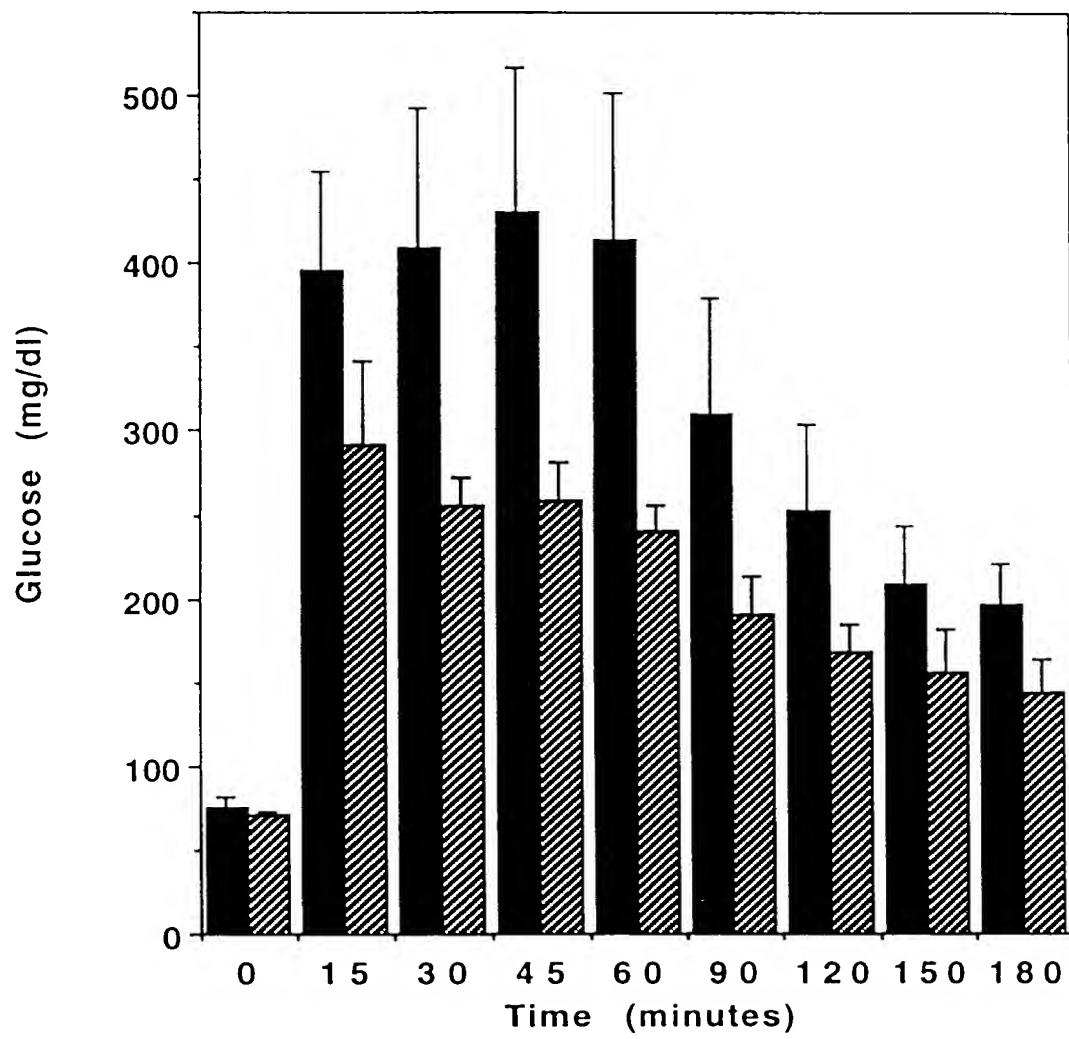


FIGURE 10